(FILE 'HOME' ENTERED AT 18:03:27 ON 24 JAN 2007)

FILE 'BIOSIS' ENTERED AT 18:03:35 ON 24 JAN 2007

L1 2 S BURKHOLDERIA CASIDAE
L2 2 S CASIDAE
L3 3258 S BURKHOLDERIA
L4 3727 S PROBIOTIC
L5 1 S L3 AND L4
L6 89323 S PSEUDOMONAS
L7 41 S L6 AND L4
L8 2144 S PSEUDOMONAS CEPACIA
L9 0 S L8 AND L4
L10 74 S PSEUDOMONAS GLADIOLI
L11 0 S L10 AND L4
L12 492849 S ADMINISTR?
L13 4 S L12 AND L7
L14 483 S BURKHOLDERIA (P)DISEASE
L15 1 S BURKHOLDERIA (P)ANIMAL DISEASE
L16 9 S BURKHOLDERIA (P)GUT

SCORE Search Results Details for Application 10776767 and Search Result 20070112_102005_us-10-776-767-1.rng.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10776767 and Search Result 20070112_102005_us-10-776-767-1.rng.

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                    GenCore version 5.1.9
                Copyright (c) 1993 - 2007  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         January 13, 2007, 13:59:11 ; Search time 1015 Seconds
                                           (without alignments)
                                           10269.469 Million cell updates/sec

Title:          US-10-776-767-1
Perfect score:  1495
Sequence:       1 AAATATTACGCTGGTTGCAT.........TATCCGAAAGTTCGGCTGGA 1495

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_8:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
                15:  geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1493.4	99.9	1495	2	AAV34335	Aav34335 Burkholde
	2	1364	91.2	1526	2	AAT01866	Aat01866 P.cepacia
	3	1348.8	90.2	1535	2	AAV24295	Aav24295 Burkholde
	4	1348.8	90.2	1535	10	ADB61689	Adb61689 16S rRNA
	5	1312.6	87.8	1488	10	ADB61690	Adb61690 16S rRNA
	6	1303	87.2	1610	10	ADB61691	Adb61691 16S rRNA
	7	1293.4	86.5	1474	2	AAT18766	Aat18766 Pseudomon
	8	1247.8	83.5	1343	15	AEF30349	Aef30349 Burkholde
	9	1242.8	83.1	1477	2	AAX26285	Aax26285 16S rDNA
	10	1192.6	79.8	1451	4	AAF74542	Aaf74542 Burkholde
	11	1192.6	79.8	1451	10	ABX10819	Abx10819 Burkholde
	12	1192.6	79.8	1451	12	ADH74483	Adh74483 TPA produ
	13	1148.4	76.8	1532	2	AAQ26729	Aaq26729 16S rRNA
	14	1148.4	76.8	1532	10	ADB61686	Adb61686 16S rRNA
	15	1135.8	76.0	1485	10	ADB61687	Adb61687 16S rRNA
	16	1135.6	76.0	1532	2	AAQ64008	Aaq64008 16S rRNA
	17	1134.6	75.9	1496	12	ADQ16355	Adq16355 Nucleotid
	18	1134.6	75.9	1496	14	AEA01071	Aea01071 Bordetell
	19	1117.8	74.8	1453	6	ABL53376	Abl53376 Escherich
	20	1117.8	74.8	1453	6	ABL53377	Abl53377 Escherich
	21	1115.8	74.6	1400	8	ABZ69300	Abz69300 J lividum
	22	1112.6	74.4	1387	3	AAA60564	Aaa60564 Vibrio sp
	23	1112.6	74.4	1400	8	ABZ69299	Abz69299 J lividum
	24	1111.4	74.3	1464	10	ADB61688	Adb61688 16S rRNA
	25	1111	74.3	1400	8	ABZ69298	Abz69298 J lividum
	26	1111	74.3	1452	2	AAX26375	Aax26375 16s rRNA
	27	1110.6	74.3	1482	8	ABZ69304	Abz69304 Janthinob
	28	1109.2	74.2	1400	8	ABZ69297	Abz69297 J lividum
	29	1107.2	74.1	1481	10	ADE11077	Ade11077 Acidovora
	30	1106.6	74.0	1509	12	ADQ67894	Adq67894 Acidovora
c	31	1104.6	73.9	1453	10	ADG44143	Adg44143 Unknown o
c	32	1104.6	73.9	1453	10	ADG17998	Adg17998 Unknown b
c	33	1104.6	73.9	1453	11	ADL27933	Adl27933 RA2 16S r
c	34	1104.6	73.9	1453	12	ADF47789	Adf47789 Unknown b
	35	1101.8	73.7	1509	12	ADQ67895	Adq67895 Acidovora
	36	1099	73.5	1530	14	ADW12666	Adw12666 Variovora
	37	1098.6	73.5	1485	4	AAC86030	Aac86030 16s rDNA,
	38	1097.2	73.4	1463	10	ADC53929	Adc53929 Phenyl hy
	39	1096.8	73.4	1495	6	ABQ78660	Abq78660 Nucleotid
	40	1090.8	73.0	1460	4	AAC86026	Aac86026 16s rDNA,
	41	1090	72.9	1343	3	AAA73019	Aaa73019 Ralstonia
c	42	1089.4	72.9	1539	10	ADG44145	Adg44145 Unknown o
c	43	1089.4	72.9	1539	10	ADG18000	Adg18000 Unknown b
c	44	1089.4	72.9	1539	11	ADL27935	Adl27935 RA6 16S r
c	45	1089.4	72.9	1539	12	ADF47791	Adf47791 Unknown b

ALIGNMENTS

RESULT 1

```
AAV34335
ID   AAV34335 standard; DNA; 1495 BP.
XX
AC   AAV34335;
XX
DT   27-AUG-2003  (revised)
DT   01-MAR-1999  (first entry)
XX
DE   Burkholderia casidae 16S rRNA gene.
XX
KW   Burkholderia casidae; 16S rRNA gene; biological control; antimicrobial;
KW   ss.
XX
OS   Burkholderia.
XX
PN   WO9848276-A1.
XX
PD   29-OCT-1998.
XX
PF   23-APR-1998;   98WO-US008148.
XX
PR   23-APR-1997;   97US-0044532P.
PR   22-APR-1998;   98US-00063898.
XX
PA   (PENN-) PENN STATE RES FOUND.
PA   (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.
XX
PI   Casida LE,  Falkinham JO,  Cain CC;
XX
DR   WPI; 1998-610004/51.
XX
PT   New isolated Burkholderia casidae bacterium - used for producing anti-
PT   microbial preparations active against bacteria, yeast, filamentous fungi,
PT   protozoa and algae.
XX
PS   Claim 67; Fig 1; 88pp; English.
XX
CC   This is the nucleotide sequence of the 16S rRNA gene of Burkholderia
CC   casidae (Bc), a novel predator bacterium that has biocontrol activity
CC   against a broad range of microorganisms, particularly microbial
CC   pathogens. Bc appears to have 5 16S rRNA operons. The DNA sequenced was a
CC   PCR product of genomic DNA from Bc strain 2.2N (ATCC 55961), generated by
CC   primers 27f (see AAV34336) and 1522r (see AAV34338). A claimed new pure
CC   culture or suspension of Bc or its variant which exhibits biocontrol
CC   activity has: (a) a 16S rRNA gene comprising a sequence that is at least
CC   97% similar to the 1495 bp sequence, and (b) a stated cellular fatty acid
CC   composition. Also claimed are: (1) a cell-free filtrate or cell fraction
CC   prepared from a pure culture or suspension as above; (2) an antimicrobial
CC   preparation comprising an alcohol extract of a cell, cyst, culture,
CC   suspension, cell-free filtrate or cell fraction of Bc; (3) a method for
CC   producing an antimicrobial preparation from Bc; and (4) a method for
CC   isolating Bc or variant on the basis of 16S rRNA sequence and cellular
CC   fatty acid composition. The pure cultures or suspensions can be used as
CC   biocontrol compositions for treating or preventing a disease of a plant
CC   (claimed) such as a disease caused by Alternaria, Aspergillus, Botrytis,
CC   Cercospora, Cercosporidium, Geotrichum, Mycosphaerella, Mucor,
CC   Penicillium, Phoma, Phytophthora, Plasmopora, Pseudopeziza, Puccinia,
CC   Pythium, Rhizoctonia, Rhizopus, Saccharomyces, Septoria, Sporothrix,
CC   Stemphylium, Trichophyton, Verticillium, Erwinia, Pseudomonas or
CC   Xanthomonas (claimed). The plants may be e.g. safflower, cotton, flax,
CC   oat, canola, poinsettia, chrysanthemum, corn, soybean, wheat, rice,
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CC   alfalfa, sorghum, peanut, tobacco, tomato, pepper, cucumber, lettuce,
CC   green bean, lima bean, pea, cantaloupe, musk melon, citrus fruit, grape,
CC   banana, geranium, azalea, rose, tulip, petunia, orchid, carnation, pine,
CC   yew or spruce (claimed). The compositions can also be used in the
CC   treatment of microbial diseases of animals, fish, humans and to control
CC   protozoan and algal growth in aquatic environments. (Updated on 27-AUG-
CC   2003 to correct OS field.)
XX
SQ   Sequence 1495 BP; 379 A; 342 C; 473 G; 301 T; 0 U; 0 Other;

  Query Match             99.9%;  Score 1493.4;  DB 2;  Length 1495;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1494;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60

Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120

Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180

Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240

Qy        241 CTACCAAGGCGACGATCAGTAGTTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTACCAAGGCGACGATCAGTAGTTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGAC 300

Qy        301 ACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTG 360
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        301 ACGGCCCAGACTCTTACGGGAGGGAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTG 360

Qy        361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420

Qy        421 AGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCT 480

Qy        481 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG 540

Qy        541 CGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGG 600

Qy        601 AACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTAG 660

Qy        661 CAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAAT 720
```

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Qy        721 ACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 780

Qy        781 GCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGCG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGCG 840

Qy        841 TGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGA 900

Qy        901 CCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACC 960

Qy        961 CTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACAG 1020

Qy       1021 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1080

Qy       1081 GCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAACC 1140

Qy       1141 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTCACACGTCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTCACACGTCA 1200

Qy       1201 TACAATGGTCGGAACAGAGGGTTGCCACCCGCGAAGGGGAGCTAATCCCAGAAAACCGAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TACAATGGTCGGAACAGAGGGTTGCCACCCGCGAAGGGGAGCTAATCCCAGAAAACCGAT 1260

Qy       1261 CGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCG 1320

Qy       1321 GATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACCATG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACCATG 1380

Qy       1381 GGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGGTAG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGGTAG 1440

Qy       1441 GATTCATGACTGGGTGAAGTCGTAACAAGTAGCCGTATCCGAAAGTTCGGCTGGA 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GATTCATGACTGGGTGAAGTCGTAACAAGTAGCCGTATCCGAAAGTTCGGCTGGA 1495
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```
RESULT 2
AAT01866
ID   AAT01866 standard; DNA; 1526 BP.
XX
AC   AAT01866;
XX
DT   16-OCT-2003  (revised)
```

```
DT   03-AUG-1999  (first entry)
XX
DE   P.cepacia 16S rRNA gene sequence.
XX
KW   16S rRNA; KK01; primer; PCR; amplification; probe; hybridisation;
KW   detection; diagnosis; ds.
XX
OS   Burkholderia cepacia.
XX
PN   JP07255486-A.
XX
PD   09-OCT-1995.
XX
PF   23-MAR-1994;   94JP-00051739.
XX
PR   23-MAR-1994;   94JP-00051739.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 1995-378541/49.
XX
PT   Pseudomonas cepacia KK01 strain 16S rRNA gene - also related probes and
PT   primers, useful for specific detection of P.cepacia strain KK01.
XX
PS   Claim 1; Page 21; 21pp; Japanese.
XX
CC   This sequence represents the 16S rRNA gene of Pseudomonas cepacia strain
CC   KK01. Fragments of the nucleic acid sequence (see AAT01872-T02316) are
CC   useful as primers and probes for the specific detection of P.cepacia
CC   strain KK01. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1526 BP; 382 A; 352 C; 486 G; 306 T; 0 U; 0 Other;

  Query Match             91.2%;  Score 1364;  DB 2;  Length 1526;
  Best Local Similarity   97.8%;  Pred. No. 0;
  Matches 1467;  Conservative    0;  Mismatches   25;  Indels    8;  Gaps    8;

Qy          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
              | ||   |||||||  |||||||||||| ||||||||||||||||||||||||||||||
Db         19 AGATTGAACGCTGGCGGCATGCCTTACA-CATGCAAGTCGAACGGCAGCACGGGTGCTTG 77

Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         78 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAAC-ATGTCCTGTAGTGGGG 136

Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 196

Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 256

Qy        241 CTACCAAGGCGACGATCAGTAG-TTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 299
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        257 CTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 316

Qy        300 CACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 359
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        317 CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 376
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Qy       360 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       377 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 436

Qy       420 AAGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC 479
            |||||||||||||| ||||||| || ||||||||||||||||||||||||||||||||||||
Db       437 AAGAAATCCTTGGCTCTAATACAGTCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC 496

Qy       480 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG 539
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       497 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG 556

Qy       540 GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG 599
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       557 GCGTAAAGCGTGCGCAGGCGGTTTGTTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG 616

Qy       600 GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA 659
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       617 GAACTGCATTGGTGACTGGCAAGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA 676

Qy       660 GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA 719
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       677 GCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA 736

Qy       720 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 779
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       737 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 796

Qy       780 CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGC 839
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       797 CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGC 856

Qy       840 GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG 899
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       857 GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG 916

Qy       900 ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       917 ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 976

Qy       960 CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1019
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       977 CCTTGACATGGTCGGAATCCTGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1036

Qy      1020 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1079
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1037 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1096

Qy      1080 CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1097 CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1156

Qy      1140 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGC-TCACACGT 1198
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      1157 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT 1216

Qy      1199 CATACAATGGTCGGAACAGAGGGTTGCC-ACCCGCGAAGGGGAGCTAATCCCAGAAAACC 1257
            |||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db      1217 CATACAATGGTCGGAACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCAGAAAACC 1276

Qy      1258 GATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1317
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                ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1277 GATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1336

Qy       1318 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACC 1377
                ||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db       1337 GCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACC 1396

Qy       1378 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGG 1437
                |||||||||||||||||||||||||||||||||||||||| || |||||| ||||||
Db       1397 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGG-AGGACGGTCACCACGG 1455

Qy       1438 TAGGATTCATGACT-GGGTGAAGTCGTAACAA-GTAGCCGTATCCGAAAGTTCGGCTGGA 1495
                |||||||||||||| |||||||||||||||| |||||||||| ||| || ||||||||
Db       1456 TAGGATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA 1515


RESULT 3
AAV24295
ID   AAV24295 standard; DNA; 1535 BP.
XX
AC   AAV24295;
XX
DT   14-SEP-1998  (first entry)
XX
DE   Burkholderia cepacia 16S ribosomal RNA gene.
XX
KW   Antibacterial; antimycobacterial; oligonucleotide; infection; therapy;
KW   ribosome binding site; Shine-Dalgarno; ribosomal RNA; cystic firbosis;
KW   tuberculosis; ss.
XX
OS   Burkholderia cepacia.
XX
PN   WO9814567-A2.
XX
PD   09-APR-1998.
XX
PF   30-SEP-1997;   97WO-US018094.
XX
PR   01-OCT-1996;   96US-0027729P.
XX
PA   (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI   Martin WJ,  Wisniowski P;
XX
DR   WPI; 1998-240079/21.
XX
PT   Use of oligo:nucleotide(s) corresponding to bacterial 16S rRNA - for
PT   inhibiting bacterial protein expression and treating bacterial infection.
XX
PS   Claim 26; Page 62-63; 73pp; English.
XX
CC   This polynucleotide comprises the 16S ribosomal RNA (rRNA) gene of
CC   Burkholderia cepacia. The invention relates to methods and compositions
CC   for the treatment of Gram-negative bacterial infections employing novel
CC   oligonucleotides as antimicrobial agents. The oligonucleotides are
CC   targeted to the Shine-Dalgarno (SD) region of prokaryotes to inhibit
CC   bacterial expression and hence inhibit bacterial infection. They
CC   preferably comprise 10-35 consecutive bases of the 3' end of a bacterial
CC   16S rRNA (see also AAV24291-94). An oligonucleotide may also include a
CC   transport moiety and may have DNA phosphate modifications to increase
CC   nuclease resistance, or may be formulated in a liposome. A claimed method
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CC   for treating a bacterial infection of a patient comprises administering a
CC   liposomal formulation of such an oligonucleotide. The oligonucleotides
CC   can be used particularly for treating bacterial infections in pulmonary
CC   diseases such as cystic fibrosis or tuberculosis. Since the SD sequence
CC   is not present in eukaryotic cells, the oligonucleotides provide a
CC   pathogen-specific therapeutic method
XX
SQ   Sequence 1535 BP; 385 A; 355 C; 488 G; 307 T; 0 U; 0 Other;

  Query Match             90.2%;  Score 1348.8;  DB 2;  Length 1535;
  Best Local Similarity   97.6%;  Pred. No. 0;
  Matches 1464;  Conservative    0;  Mismatches   27;  Indels    9;  Gaps    9;

Qy          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
              | ||   ||||||| |||||| | ||| ||||||||||||||||||||||||||||||
Db         27 AGATTGAACGCTGGCGGCATGCTTAACA-CATGCAAGTCGAACGGCAGCACGGGTGCTTG 85

Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         86 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAAC-ATGTCCTGTAGTGGGG 144

Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 204

Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        205 TTCGGGCCTCGCGCTATAGGGTTGG-CGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 263

Qy        241 CTACCAAGGCGACGATCAGTAG-TTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 299
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db        264 CTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 323

Qy        300 CACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 359
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        324 CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 383

Qy        360 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 443

Qy        420 AAGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC 479
              ||||||||| ||| ||||||| || ||||||||||||||||||||||||||||||||||||
Db        444 AAGAAATCCCTGGCTCTAATACAGTCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC 503

Qy        480 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG 539
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        504 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG 563

Qy        540 GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG 599
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG 623

Qy        600 GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA 659
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA 683

Qy        660 GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA 719
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        684 GCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA 743
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Qy        720 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 803

Qy        780 CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGC 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGC 863

Qy        840 GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG 923

Qy        900 ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 983

Qy        960 CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1019
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        984 CCTTGACATGGTCGGAATCCTGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1043

Qy       1020 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1103

Qy       1080 CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1163

Qy       1140 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGC-TCACACGT 1198
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1164 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT 1223

Qy       1199 CATACAATGGTCGGAACAGAGGGTTGCC-ACCCGCGAAGGGGAGCTAATCCCAGAAAACC 1257
              |||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db       1224 CATACAATGGTCGGAACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCAGAAAACC 1283

Qy       1258 GATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1317
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1284 CATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1343

Qy       1318 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACC 1377
              |||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||
Db       1344 GCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACC 1403

Qy       1378 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGG 1437
              |||||||||||||||||||||||||||||||||||||||||||| || |||||| ||||||
Db       1404 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGG-AGGACGGTCACCACGG 1462

Qy       1438 TAGGATTCATGACT-GGGTGAAGTCGTAACAA-GTAGCCGTATCCGAAAGTTCGGCTGGA 1495
              |||||||||||||| |||||||||||||||| |||||||||| ||| || ||||||||
Db       1463 TAGGATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA 1522
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RESULT 4
ADB61689
ID   ADB61689 standard; DNA; 1535 BP.
XX
AC   ADB61689;
XX
DT   04-DEC-2003  (first entry)
XX
```

DE 16S rRNA of Burkholderia cepacia DNA sequence.
XX
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS Burkholderia cepacia.
XX
PN WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029397.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
DR WPI; 2003-663255/62.
XX
PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.
XX
PS Claim 4; Page 173-174; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Burkholderia cepacia related to
CC the invention.
XX
SQ Sequence 1535 BP; 385 A; 355 C; 488 G; 307 T; 0 U; 0 Other;

Query Match 90.2%; Score 1348.8; DB 10; Length 1535;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 27; Indels 9; Gaps 9;

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Qy          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
              | ||   |||||||  ||||||  | ||| ||||||||||||||||||||||||||||||
Db         27 AGATTGAACGCTGGCGGCATGCTTAACA-CATGCAAGTCGAACGGCAGCACGGGTGCTTG 85

Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         86 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAAC-ATGTCCTGTAGTGGGG 144

Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 204

Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        205 TTCGGGCCTCGCGCTATAGGGTTGG-CGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 263

Qy        241 CTACCAAGGCGACGATCAGTAG-TTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 299
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db        264 CTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 323

Qy        300 CACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 359
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        324 CACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 383

Qy        360 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 443

Qy        420 AAGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC 479
              |||||||| ||| ||||||| || ||||||||||||||||||||||||||||||||||||
Db        444 AAGAAATCCCTGGCTCTAATACAGTCGGGGGATGACGGTACCGGAAGAATAAGCACCGGC 503

Qy        480 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGG 539
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        504 TAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGG 563

Qy        540 GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGG 623

Qy        600 GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GAACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTA 683

Qy        660 GCAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA 719
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        684 GCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAA 743

Qy        720 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA 803

Qy        780 CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGC 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGC 863

Qy        840 GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 GTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGG 923

Qy        900 ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 959
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         924 ACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTAC 983

Qy         960 CCTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1019
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         984 CCTTGACATGGTCGGAATCCTGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACA 1043

Qy        1020 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1079
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1044 GGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1103

Qy        1080 CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1139
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1104 CGCAACCCTTGTCCTTAGTTGCTACGCAAGAGCACTCTAAGGAGACTGCCGGTGACAAAC 1163

Qy        1140 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGC-TCACACGT 1198
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        1164 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTCACACGT 1223

Qy        1199 CATACAATGGTCGGAACAGAGGGTTGCC-ACCCGCGAAGGGGAGCTAATCCCAGAAAACC 1257
                |||||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Db        1224 CATACAATGGTCGGAACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCCAGAAAACC 1283

Qy        1258 GATCGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1317
                 |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        1284 CATCGTAGTCCGGATTGCACTCTGCAACTCGAGTGCATGAAGCTGGAATCGCTAGTAATC 1343

Qy        1318 GCGGATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACC 1377
                ||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||
Db        1344 GCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACC 1403

Qy        1378 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGG 1437
                |||||||||||||||||||||||||||||||||||||||||||| || |||||| ||||||
Db        1404 ATGGGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGG-AGGACGGTCACCACGG 1462

Qy        1438 TAGGATTCATGACT-GGGTGAAGTCGTAACAA-GTAGCCGTATCCGAAAGTTCGGCTGGA 1495
                |||||||||||||| |||||||||||||||| |||||||||| ||| || ||||||||
Db        1463 TAGGATTCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA 1522
```

```
RESULT 5
ADB61690
ID   ADB61690 standard; DNA; 1488 BP.
XX
AC   ADB61690;
XX
DT   04-DEC-2003  (first entry)
XX
DE   16S rRNA of Burkholderia mallei DNA sequence.
XX
KW   enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW   poly-A tail; mRNA purification; oligo-dT capture;
KW   prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW   capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW   eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW   28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS   Burkholderia mallei.
XX
PN   WO2003054162-A2.
XX
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PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029397.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
DR WPI; 2003-663255/62.
XX
PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.
XX
PS Claim 4; Page 174; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Burkholderia mallei related to the
CC invention.
XX
SQ Sequence 1488 BP; 373 A; 344 C; 480 G; 291 T; 0 U; 0 Other;

Query Match 87.8%; Score 1312.6; DB 10; Length 1488;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 44; Indels 10; Gaps 9;

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Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
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Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
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Db        117 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTGAGGATGAAAGCGGGGGACC 176

Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
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Qy        241 CTACCAAGGCGACGATCAGTAG-TTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGA 299
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Qy        300 CACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCT 359
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Qy        360 GATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGA 419
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RESULT 6
ADB61691
ID   ADB61691 standard; DNA; 1610 BP.
XX
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DT   04-DEC-2003  (first entry)
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DE   16S rRNA of Burkholderia pseudomallei DNA sequence.
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KW   enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW   poly-A tail; mRNA purification; oligo-dT capture;
KW   prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW   capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW   eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW   28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS   Burkholderia pseudomallei.
XX
PN   WO2003054162-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US041014.
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PR   20-DEC-2001; 2001US-00029397.
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PA   (AMBI-) AMBION INC.
XX
PI   Murphy GL,  Whitley JP;
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DR   WPI; 2003-663255/62.
XX
PT   Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
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PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.
XX
PS Claim 4; Page 175; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Burkholderia pseudomallei related
CC to the invention.
XX
SQ Sequence 1610 BP; 394 A; 383 C; 514 G; 319 T; 0 U; 0 Other;

Query Match 87.2%; Score 1303; DB 10; Length 1610;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1419; Conservative 0; Mismatches 45; Indels 9; Gaps 8;

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Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
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start | next page

SCORE Search Results Details for Application 10776767 and Search Result 20070112_102015_us-10-776-767-1.rnpm.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10776767 and Search Result 20070112_102015_us-10-776-767-1.rnpm.

start | next page

Go Back to previous page

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: January 13, 2007, 15:19:33 ; Search time 7967 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 173069072

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	6	1348.8	90.2	1535	39	US-10-029-397A-41	Sequence 41, Appl
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c	33	1104.6	73.9	1453	78	US-60-171-140-4	Sequence 4, Appli
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	36	1099	73.5	1530	83	US-60-499-622-1	Sequence 1, Appli
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	39	1095	73.2	1452	18	US-08-965-623-2	Sequence 2, Appli
	40	1095	73.2	1526	70	US-11-198-242-1	Sequence 1, Appli
	41	1090.8	73.0	1460	41	US-10-168-337A-6	Sequence 6, Appli

SCORE Search Results Details for Application 1(Result 20070112_102007_us-10-776-

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10776767 and Search Result 2007011
start | next page

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

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10869.971 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	1367.2	91.5	110000	15	CP000151_05	Continuation (6 of
15	1366	91.4	1484	15	AY741352	AY741352 Burkholde
16	1365.6	91.3	1528	15	AB114607	AB114607 Burkholde
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35	1358.4	90.9	1485	15	AY741343	AY741343 Burkholde
36	1358.4	90.9	1485	15	BSP420880	AJ420880 Burkholde
37	1358.2	90.8	1488	15	AY741332	AY741332 Burkholde
38	1358	90.8	1480	15	AB008002	AB008002 Burkholde
39	1357.6	90.8	1497	15	AY741361	AY741361 Burkholde
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43	1357	90.8	1494	15	AF311970	AF311970 Burkholde
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ALIGNMENTS

RESULT 1
AR178244
LOCUS AR178244 1495 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6319497.
ACCESSION AR178244

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VERSION     AR178244.1  GI:20219382
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1495)
  AUTHORS   Casida,L.Earl. Jr., Falkinham,J.Oliver. III and Cain,C.Christopher.
  TITLE     Non-obligate predatory bacterium burkholderia casidaeand uses
            thereof
  JOURNAL   Patent: US 6319497-A 1 20-NOV-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 1495;  DB 2;  Length 1495;
  Best Local Similarity  100.0%;  Pred. No. 1.4;
  Matches 1495;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
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Db        361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420

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Db        781 GCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGCG 840

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Db       1141 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTCACACGTCA 1200

Qy       1201 TACAATGGTCGGAACAGAGGGTTGCCACCCGCGAAGGGGAGCTAATCCCAGAAAACCGAT 1260
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Db       1201 TACAATGGTCGGAACAGAGGGTTGCCACCCGCGAAGGGGAGCTAATCCCAGAAAACCGAT 1260

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RESULT 2
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LOCUS       AR473471               1495 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 1 from patent US 6689357.
ACCESSION   AR473471
VERSION     AR473471.1  GI:42708950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1495)
  AUTHORS   Casida,L.E. Jr., Falkinham,J.O. III and Cain,C.C.
  TITLE     Non-obligate predatory bacterium Burkholderia casidae and uses
            thereof
  JOURNAL   Patent: US 6689357-A 1 10-FEB-2004;
            Virginia Tech Intellectual Properties, Inc. and The Penn State
            Research Foundation; Blacksburg, VA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1495;  DB 2;  Length 1495;
  Best Local Similarity  100.0%;  Pred. No. 1.4;
  Matches 1495;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
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Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
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Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
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Db        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180

Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
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Qy        241 CTACCAAGGCGACGATCAGTAGTTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGAC 300
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Db        241 CTACCAAGGCGACGATCAGTAGTTGTCTGAGAGGACGACCAGCCACACTGGGACTGAGAC 300

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Db        301 ACGGCCCAGACTCTTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTG 360

Qy        361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420
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Db        361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420

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Qy       541 CGTAAAGCGTGCGCAGGCGGTTTGCTAAGACCGATGTGAAATCCCCGGGCTCAACCTGGG 600
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Db       781 GCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGCG 840

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Db       841 TGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGA 900

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Db       961 CTTGACATGGTCGGAATCCCGCTGAGAGGTGGGAGTGCTCGAAAGAGAACCGGCGCACAG 1020

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Qy       1441 GATTCATGACTGGGTGAAGTCGTAACAAGTAGCCGTATCCGAAAGTTCGGCTGGA 1495
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RESULT 3
AF226727
LOCUS       AF226727                1495 bp    DNA     linear   BCT 13-SEP-2000
DEFINITION  Burkholderia sp. casida 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF226727
VERSION     AF226727.1  GI:7107388
KEYWORDS    .
SOURCE      Burkholderia sp. casida
  ORGANISM  Burkholderia sp. casida
            Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
            Burkholderiaceae; Burkholderia.
REFERENCE   1  (bases 1 to 1495)
  AUTHORS   Cain,C.C., Henry,A.T., Waldo,R.H. III, Casida,L.J. Jr. and
            Falkinham,J.O. III.
  TITLE     Identification and characteristics of a novel Burkholderia strain
            with broad-spectrum antimicrobial activity
  JOURNAL   Appl. Environ. Microbiol. 66 (9), 4139-4141 (2000)
   PUBMED   10966443
REFERENCE   2  (bases 1 to 1495)
  AUTHORS   Cain,C.C. and Falkinham,J.O. III.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2000) Biology, Virginia Tech, Fralin
            Biotechnology Center, Blacksburg, VA 24061-0346, USA
FEATURES             Location/Qualifiers
     source          1. .1495
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches 1495;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AAATATTACGCTGGTTGCATGCCTTACAGCATGCAAGTCGAACGGCAGCACGGGTGCTTG 60
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Qy         61 CACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACAATGTCCTGTAGTGGGG 120
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Qy        121 GATAGCCCGGCGAAAGCCGGATTAATACCGCATACGATCTACGGATGAAAGCGGGGGACC 180
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Qy        181 TTCGGGCCTCGCGCTATAGGGTTGGCCGATGGCTGATTAGCTAGTTGGTGGGGTAAAGGC 240
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Qy       361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420
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Db       361 ATCCAGCAATGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTGTCCGGAA 420

Qy       421 AGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCT 480
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Db       421 AGAAATCCTTGGTTCTAATATAGCCGGGGGATGACGGTACCGGAAGAATAAGCACCGGCT 480

Qy       481 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG 540
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Db       481 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGG 540

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Db       601 AACTGCATTGGTGACTGGCAGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCACGTGTAG 660

Qy       661 CAGTGAAATGCGTAGAGATGTGGAAGAATACCGATGGCGAAGGCAGCCCCCTGGGCCAAT 720
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Qy       781 GCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGCG 840
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Qy       841 TGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGA 900
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Qy       901 CCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACC 960
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Qy      1021 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1080
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Qy      1141 GGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTCACACGTCA 1200
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Qy       1261 CGTAGTCCGGATTGCACTCTGCACCTCGAGTGCATGAAGCTGGAATCGCTAGTAATCGCG 1320
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Qy       1321 GATCAGCATGCCGCGGTGAATACTTTCCCGGGTTTTGTACACACCGCCCGTCACACCATG 1380
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Qy       1381 GGAGTGGGTTTTACCAGAAGTGGCTAGTCTAACCGCAAGGAAGAACGGTCCCCACGGTAG 1440
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BSP491304
LOCUS       BSP491304               1523 bp    DNA     linear   BCT 18-JUN-2003
DEFINITION  Burkholderia sp. CEB01056 16S rRNA gene, strain CEB01056.
ACCESSION   AJ491304
VERSION     AJ491304.1  GI:31873152
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Burkholderia sp. CEB01056
  ORGANISM  Burkholderia sp. CEB01056
            Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
            Burkholderiaceae; Burkholderia.
REFERENCE   1
  AUTHORS   Ramisse,V., Balandreau,J., Thibault,F., Vidal,D., Vergnaud,G. and
            Normand,P.
  TITLE     DNA-DNA hybridization study of Burkholderia species using genomic
            DNA macro-array analysis coupled to reverse genome probing
  JOURNAL   Int. J. Syst. Evol. Microbiol. 53 (Pt 3), 739-746 (2003)
   PUBMED   12807195
REFERENCE   2  (bases 1 to 1523)
  AUTHORS   Ramisse,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUN-2002) Ramisse V., Microbiologie, Centre d'Etudes
            du Bouchet, BP3, 91710 Vert le Petit, FRANCE
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SCORE Search Results Details for Application 10776767 and Search Result 20070112_102010_us-10-776-767-1.rst.

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This page gives you Search Results detail for the Application 10776767 and Search Result 20070112_102010_us-10-776-767-1.rst.

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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: January 13, 2007, 14:51:42 ; Search time 7704 Seconds
(without alignments)
10851.428 Million cell updates/sec

Title: US-10-776-767-1
Perfect score: 1495
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	671.6	44.9	1143	11	BH814966	BH814966 pBPC15 Ma
	3	648.6	43.4	1954	8	CX109203	CX109203 RECm0593
	4	615.4	41.2	941	5	CK296497	CK296497 EST759211
	5	587.6	39.3	1084	11	BZ439740	BZ439740 BONDU54TF
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	7	580	38.8	1033	14	DU743187	DU743187 ASNC1602.
	8	579	38.7	889	5	CK280527	CK280527 EST743249
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c	14	562.4	37.6	1031	11	BH656222	BH656222 BOMJZ86TF
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	17	558.2	37.3	746	11	AQ957362	AQ957362 LERAP36TF
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c	19	555.2	37.1	1016	11	BZ426201	BZ426201 BONDZ28TF
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	29	527	35.3	974	11	BZ440868	BZ440868 BONKT51TR
	30	521.6	34.9	860	8	CN757363	CN757363 ID0AAA1CE
c	31	521	34.8	924	13	DU101928	DU101928 JBnY023N1
	32	520.8	34.8	861	14	DU486180	DU486180 109842109
	33	519	34.7	951	11	BH651765	BH651765 BOMFE30TR
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ALIGNMENTS

RESULT 1
BH771024

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This page gives you Search Results detail for the Application 10776767 and Search Result 20070112_102013_us-10-776-767-1.rni.

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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

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(without alignments)
10246.548 Million cell updates/sec

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Perfect score: 1495
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5		1192.6	79.8	1451	3	US-09-617-854A-1	Sequence 1, Appli
6	c	1104.6	73.9	1453	3	US-09-735-567-4	Sequence 4, Appli
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13		1065.6	71.3	1455	2	US-08-642-229A-3	Sequence 3, Appli
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18		940.6	62.9	1484	2	US-08-632-470-53	Sequence 53, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09063898
; Patent No. 6319497
; GENERAL INFORMATION:
; APPLICANT: Casida, Jr., Lester E.

SCORE Search Results Details for Application 10776767 and Search Result 20070112_102021_us-10-776-767-1.rnpbm.

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                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2007  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         January 13, 2007, 15:27:11 ; Search time 2057 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2		1495	100.0	1495	8	US-10-776-767-1	Sequence 1, Appli
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5		1303	87.2	1610	7	US-10-029-397A-43	Sequence 43, Appl
6		1268.4	84.8	1522	16	US-11-198-242-2	Sequence 2, Appli
7		1192.6	79.8	1451	7	US-10-219-549-1	Sequence 1, Appli
8		1148.4	76.8	1532	7	US-10-029-397A-38	Sequence 38, Appl
9		1135.8	76.0	1485	7	US-10-029-397A-39	Sequence 39, Appl
10		1134.6	75.9	1496	10	US-10-723-365B-32	Sequence 32, Appl
11		1111.4	74.3	1464	7	US-10-029-397A-40	Sequence 40, Appl
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18		1098.6	73.5	1485	7	US-10-168-337A-10	Sequence 10, Appl
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23	c	1089.4	72.9	1539	7	US-10-464-709-6	Sequence 6, Appli
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27		1083.2	72.5	1454	7	US-10-464-724-7	Sequence 7, Appli
28		1083.2	72.5	1454	7	US-10-464-356-7	Sequence 7, Appli
29		1083.2	72.5	1454	7	US-10-464-709-7	Sequence 7, Appli
30		1082.4	72.4	1460	7	US-10-168-337A-4	Sequence 4, Appli
31		1080.4	72.3	1458	8	US-10-659-948A-3	Sequence 3, Appli
32		1080.4	72.3	1458	8	US-10-659-980A-3	Sequence 3, Appli
33		1080.4	72.3	1458	8	US-10-659-983A-3	Sequence 3, Appli
34		1078.4	72.1	1459	7	US-10-168-337A-8	Sequence 8, Appli
35		1078	72.1	1478	7	US-10-168-337A-3	Sequence 3, Appli
36		1077.8	72.1	1491	8	US-10-659-948A-20	Sequence 20, Appl
37		1077.8	72.1	1491	8	US-10-659-980A-20	Sequence 20, Appl
38		1077.8	72.1	1491	8	US-10-659-983A-20	Sequence 20, Appl
39		1076.6	72.0	1405	11	US-10-515-311-5	Sequence 5, Appli
40		1075.4	71.9	1426	7	US-10-168-337A-9	Sequence 9, Appli
41		1072.8	71.8	1460	7	US-10-168-337A-2	Sequence 2, Appli
42		1071.8	71.7	1460	7	US-10-168-337A-1	Sequence 1, Appli
43		1060.8	71.0	1457	8	US-10-659-948A-1	Sequence 1, Appli
44		1060.8	71.0	1457	8	US-10-659-980A-1	Sequence 1, Appli
45		1060.8	71.0	1457	8	US-10-659-983A-1	Sequence 1, Appli

ALIGNMENTS